

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: de la Monte, Suzanne
Wands, Jack R.

(ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Esmond, Robert W.
(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 0609.4370000

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTG TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC
Met Glu Phe Ser Leu Leu Pro Arg Leu Glu Cys
1 5 10

50

AAT	GGC	GCA	ATC	TCA	GCT	CAC	CGC	AAC	CTC	CGC	CTC	CCG	GGT	TCA	AGC	98
Asn	Gly	Ala	Ile	Ser	Ala	His	Arg	Asn	Leu	Arg	Leu	Pro	Gly	Ser	Ser	
15									20					25		
GAT	TCT	CCT	GCC	TCA	GCC	TCC	CCA	GTA	GCT	GGG	ATT	ACA	GGC	ATG	TGC	146
Asp	Ser	Pro	Ala	Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Gly	Met	Cys	
30									35					40		
ACC	CAC	GCT	CGG	CTA	ATT	TTG	TAT	TTT	TTA	GTA	GAG	ATG	GAG	TTT		194
Thr	His	Ala	Arg	Leu	Ile	Leu	Tyr	Phe	Phe	Leu	Val	Glu	Met	Glu	Phe	
45									50					55		60
CTC	CAT	GTT	GGT	CAG	GCT	GGT	CTC	GAA	CTC	CCG	ACC	TCA	GAT	GAT	CCC	242
Leu	His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Pro	Thr	Ser	Asp	Asp	Pro	
65									70					75		
TCC	GTC	TCG	GCC	TCC	CAA	AGT	GCT	AGA	TAC	AGG	ACT	GGC	CAC	CAT	GCC	290
Ser	Val	Ser	Ala	Ser	Gln	Ser	Ala	Arg	Tyr	Arg	Thr	Gly	His	His	Ala	
80									85					90		
CGG	CTC	TGC	CTG	GCT	ATT	TTT	TGT	GGT	AGA	AAC	AGG	GTT	TCA	CTG	ATG	338
Arg	Leu	Cys	Leu	Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	
95									100					105		
TGC	CCA	AGC	TGG	TCT	GAG	CTC	AAG	CAG	TCC	ACC	TGC	CTC	AGC	CTC		386
Cys	Pro	Ser	Trp	Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu	
110									115					120		
CCA	AAG	TGC	TGG	GAT	TAC	AGG	CGT	GCA	GCC	GTG	CCT	GGC	CTT	TTT	ATT	434
Pro	Lys	Cys	Trp	Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile	
125									130					135		140
TTC	TTT	TTT	TTA	AGA	CAC	AGG	TGT	CCC	ACT	CTT	ACC	CAG	GAT	GAA	GTG	482
Leu	Phe	Phe	Leu	Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val	
145									150					155		
CAG	TGG	TGT	GAT	CAC	AGC	TCA	CTG	CAG	CCT	TCA	ACT	CCT	GAG	ATC	AAG	530
Gln	Trp	Cys	Asp	His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	
160									165					170		
CAT	CCT	CCT	GCC	TCA	GCC	TCC	CAA	GTA	GCT	GGG	ACC	AAA	GAC	ATG	CAC	578
His	Pro	Pro	Ala	Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His	
175									180					185		
CAC	TAC	ACC	TGG	CTA	ATT	TTT	ATT	TTT	ATT	TTT	AAT	TTT	TTG	AGA	CAG	626
His	Tyr	Thr	Trp	Leu	Ile	Phe	Ile	Phe	Ile	Phe	Asn	Phe	Leu	Arg	Gln	
190									195					200		
AGT	CTC	AAC	TCT	GTC	ACC	CAG	GCT	GGA	GTG	CAG	TGG	CGC	AAT	CTT	GGC	674
Ser	Leu	Asn	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Arg	Asn	Leu	Gly	
205									210					215		220
TCA	CTG	CAA	CCT	CTG	CCT	CCC	GGG	TTC	AAG	TTA	TTC	TCC	TGC	CCC	AGC	722
Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Phe	Lys	Leu	Phe	Ser	Cys	Pro	Ser	
225									230					235		
CTC	CTG	AGT	AGC	TGG	GAC	TAC	AGG	CGC	CCA	CCA	CGC	CTA	GCT	AAT	TTT	770
Leu	Leu	Ser	Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe		
240									245					250		
TTT	GTA	TTT	TTA	GTA	GAG	ATG	GGG	TTC	ACC	ATG	TTC	GCC	AGG	TTG	ATC	818
Phe	Val	Phe	Leu	Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile	
255									260					265		
TTG	ATC	TCT	GGA	CCT	TGT	GAT	CTG	CCT	GCC	TCC	CAA	AGT	GCT			866

09954557 - 092601

Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala			
270	275	280	
GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT			914
Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys			
285	290	295	300
TTG TTT GAA ATG TCT CAC TCT GTT ACC CAG CCT GGA GTG CAA TGG			962
Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp			
305	310	315	
CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC			1010
Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe			
320	325	330	
TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA			1058
Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro			
335	340	345	
CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT			1106
His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr			
350	355	360	
TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT			1159
Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg			
365	370	375	
TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCGGCTAAAT TTAGATAAAA			1219
AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TTGTCCTAAA CTTCTGGCTT			1279
CATGCAATCC TTCCAAATGA GCCACAAACAC CCAGCCAGTC ACATTTTTTA AACAGTTACA			1339
TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACTGTC AAATTCAGTA			1399
GTAACAGAGT TCTTTATAA CTTTTAAACA AAGCTTTAGA GCA			1442

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Ser Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile			
1	5	10	15
Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala			
20	25	30	
Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg			
35	40	45	
Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly			
50	55	60	
Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala			
65	70	75	80
Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu			

85

90

95

Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
100 105 110

Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
115 120 125

Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
130 135 140

Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
145 150 155 160

His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
165 170 175

Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
180 185 190

Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
195 200 205

Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
210 215 220

Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
225 230 235 240

Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
245 250 255

Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
260 265 270

Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
275 280 285

Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
290 295 300

Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
305 310 315 320

Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
325 330 335

Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
340 345 350

Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
355 360 365

Ser Gln Thr Pro Asp Leu Arg
370 375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTT GAGATGGAGT	TTTCGCTCTT	GTGCCCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGGGAT	TCTCCCTGCCT	120
AGTAGCTGGG	ATTACAGGCA	TGTGCACCA	GCTCGGCTAA	TTTTGTATTT	180
GAGATGGAGT	TTAACTCCAT	GTGGTCAGG	CTGGTCTCGA	ACTCCCGACC	240
TCCCGTCTCG	GCCTGCCAA	AGTGCAGAGA	TTACAGGCAT	GAGCCACCAT	300
TGCGCTGGCTA	ATTTTGTGG	TAGAACAGG	GTTCACTGA	TGTTGCCAA	360
TGAGCTCAAG	CAGTCCACCT	GCCTCAGCCT	CCCAAAGTGC	TGGGATTACA	420
GTGCCTGGCC	TTTTTATTTT	ATTTTTTTA	AGACACAGGT	GTACCACTCT	480
GAAGTGCAGT	GGTGTGATCA	CAGCTCACTG	CAGCCTCAA	CTCCGTGAGAT	540
TCCTGCCTCA	GCCTCCCAAG	TAGCTGGAC	CAAAGACATG	CACCACTACA	600
TTTATTTTTA	TTTTAAATT	TTTGAGACAG	AGTCTCACTC	TGTCACCCAG	660
AGTGGCCAA	TCTTGGCTCA	CTGCAACCTC	TGCGCTCCCG	GTCAAGTTA	720
CCAGCCTCCT	GAGTAGCTGG	GACTACAGGC	GCCCCACACG	CCTAGCTAAT	780
TTTTAGTAGA	GATGGGGTTT	CACCATGTT	GCCAGGTTGA	TCTTGATCTC	840
GATCTGCCTG	CCTCGGCCTA	CCCAAAGTGC	TGGGATTACA	GGTCGTGACT	900
CTATTTTTAA	TTTTGTTTG	TTTGAAATGG	AATCTCACTC	TGTTACCCAG	960
AATGGCAAAT	CTCGGCTACT	CGCAACCTCT	GCCTCCCGGG	TCAAGCGATT	1020
AGCCTCCAA	GCAGCTGGGA	TTACGGGACC	TGCAACACAC	CCCGCTAATT	1080
CATTAGAGGC	GGGTTTACCA	TATTTGTCAG	GCTGGGTCTC	AAACTCCTGA	1140
CCCACCTGCC	TCAGCCTTCC	AAAGTGCCTGG	GATTACAGGC	GTGAGCCACC	1200
GGCTAATTG	GAATAAAAAA	TATGTAGCAA	TGGGGGTCTG	CTATGTTGCC	1260
TCAAACCTCT	GGCTTCAGTC	AATCCCTCCA	AATGAGCCAC	AACACCCAGC	1320
TTTTAAACAG	TTACATCTT	ATTTTAGTAT	ACTAGAAAAGT	AATAACAATAA	1380
C					1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTTT	GAGATGGAGT	TTTCGCTCTT	GTTGCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
AGTAGGCTGG	GATTACAGGC	ATGTGCACCA	CGCTCGGCTA	ATTTTGATATT	TTTTTTAGT	180
AGAGATGGAG	TTTCTCCATG	TTGGTCAGGC	TGGTCTCGAA	CTCCGACCTC	AGATGATCCT	240
CCCGTCTCGG	CCTCCCAAAG	TGCTAGATAC	AGGACTGAGC	ACCATGCCCG	GCCTCTGCCT	300
GGCTAATTTT	TGTGGTAGAA	ACAGGGTTTC	ACTGATGTGC	CCAAGCTGGT	CTCCTGAGCT	360
CAAGCAGTCC	ACCTGCTCA	GCCTCCAAA	GTGCTGGAT	TACAGGCGTG	CAGCCGTGCC	420
TGGCCTTTTT	ATTTTATTTT	TTTTAAGACA	CAGGGTGTCCC	ACTCTTACCC	AGGATGAAGT	480
GCAGTGGTGT	GATCACAGCT	CACTGCAGCC	TTCAACTCTG	AGATCAAGCA	TCCTCTGCC	540
TCAGCCTCCC	AAAGTAGCTG	GGACCAAAGA	CATGCACCC	TACACCTGGC	TAATTTTAT	600
TTTTATTTTT	ATTTTTTGA	GACAGAGTCT	CAACTCTGTC	ACCCAGGCTG	GAGTGCAGTG	660
GGCCTAATCTT	GGCTCACTGC	AACCTCTGCC	TCCCGGGTTC	AAAGTTATCT	CCTGCCCGAG	720
CCTCCTGAGT	AGCTGGGACT	ACAGGCGCCC	ACCACGCC	GCTAATTTTT	TTGTATTTT	780
AGTAGAGATG	GGGTTTCACC	ATGTTGCA	GGTTGATGCT	AGATCTCTTG	ACCTTGTGAT	840
CTGCCTGCT	CGGCCCTCCA	AAAGTGTGGG	ATTACAGGAC	GTGACGCCA	CCGCCCGGCC	900
TATTTTAAT	TTTTGTTGT	TTGAAATGGA	ATCTCACTCT	GTTACCCAGG	CTGGAGTGCA	960
ATGGCCAAT	CTCGGCTCAC	TGCAACCTCT	GCCTCCCGGG	CTCAAGCGAT	TCTCCTGTCT	1020
CAGCCTCCC	AGCAGCTGGG	ATTACGGCA	CCTGCACCC	ACCCCGCTAA	TTTTTGATTT	1080
TTCATTAGAG	GGGGGGTTTC	ACCATAATTG	TCAGGCTGGT	CTCAAACCTCC	TGACCTCAGG	1140
TGACCCACCT	GCCTCAGCCT	TCCAAAGTGC	TGGGATTACA	GGCGTGACCG	CTCACCCAGC	1200
CGGCTAATTT	AGATAAAAAA	ATATGTTGCA	ATGGGGGGTC	TTGCTATGTT	GCCCAGGCTG	1260
GTCTCAAAC	TCTGGCTTC	TGCAATCCTT	CCAAATGAGC	CACAACACCC	AGCCAGTCAC	1320
ATTTTTAAC	AGTTACATCT	TTATTTAGT	ATATAGAAA	GTGATACGAT	AAACATGGCGG	1380
AACCTGCAAA	TTCGAGTAGT	ACAGAGTCTT	TTATAACT			1418

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

0996467-008260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACCTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14